

SEQUENCES OF SELECTED REGIONS OF APTAMERS AGAINST D-AMINO ACID A β 1-40 TARGETS 1,2,3

5 Target 1 (MONOMERIC)

SEQ ID NO:1

GGA CGA AGA GCG TTA TCT TAC GCT GAC TGG ATA TTA GTT TGT TGG AAT AC

10

SEQ ID NO:2

TCG TTA TTC TGT TCA GGG TTT GAG ACT CGT TGT ATC GAT TTA G... .

15 SEQ ID NO:3

GGC CCC TAT ACG AAC GTC ATC GTA CTC AGC TGT TGT TGT CC. . . .

SEQ ID NO:4

20 TTT ATA TCG CTT CCA CGT GTT TTA CCC ACA CCT TGT TTT AGC GGT AA. .

SEQ ID NO:5

25 TTA ATG ACG CTG TAC ATG GGA TCG TAT AGT GCC ACA GGT AAA TCT GCA TG

SEQ ID NO:6

CTG TTC TTA TCA AGC CAA ATA AAG TAC TAT GCC CTA AGG CCT ATA TGA TC

30

SEQ ID NO:7

CGG TGG GAA ATA TCT TTG GCT GGC TTA GTA ACT TCG TAT TTG CTC GGC TG

35 SEQ ID NO:8

TTG TCC ATT GTA TAC GAT GCG CTT CAA GGA TGA TAC GGC TTT CAC GCA ..

SEQ ID NO:9

40 TCC CTT AGC AGG CTT CAT TTC CTT GAC CAT TCT TTG CGT TGA GCC TGT CT

SEQ ID NO:10

AAA CGA GTA TCT TTT TGG GAT CTT TCA GCT GCT AGT GCA ATA TCA TCT CT

5

SEQ ID NO:12

TGG TCC TGC GAC CAG CAG TCA ATT AGG GTT TAG CAC AGT AGA GGC CT.

0

SEQ ID NO:13

CGC GAC TAA CTT GCG TCA GTT TTG TAC GGG TGT TTA GCT CCC TTT TA.

5

SEQ ID NO:14

TTC TCT CAC TTC CTT CCA GGT GAA CGG CGC ATT AAG GTC TTG TTG AT...

:0

SEQ ID NO:15

CAG AGT TAG ATG GCA GCT ATT GTC GCC TAAGTT TGC TTT ATA TCA TCT TT

:5

SEQ ID NO:16

CGG CGC GTC CCT GCA AGT CAA CTG TTT CCT GGC TCG CTT TAC GAT

CCT TT

Target 2 (PRE-FIBRILLAR)

SEQ ID NO:17

CGT ACA CAT CAA ACT TTC GAA TCC ACA GGA TAA TCG AGG AGA TCT CCT GA

5

SEQ ID NO:18

TTG TCG CGA TAC TAC ATT TGT CCT GTC TGT GTG TCA TAC GGA ACT
GTG TA

10

SEQ ID NO:19

CGC CCG TCG ATT TGA AAC ACT CTT CAT CGG CGT TAA CCA CGG CGT GGA GA

15

SEQ ID NO:20

CGT ACC GCG CTA CGT TCC CAT AAG CGT GCA ATT TGT TTG CCT TGG GTT GG

20

SEQ ID NO:21

CTT TCA AGG TGG GGA TAC CGA GAC AAT TAG TCA TCT GTA GTGT GAT CAG T.

SEQ ID NO:22

25

TAG AAG CGT CGA ATC ATT GGG AAT TCG TGC ATT TAG GGC AGG CAC TTT GG

SEQ ID NO:23

CAA GCG AAA TGT CAC TGT GTA AGG TGT AAC AGG GAA CAA GGG AGG ACA A.

30

SEQ ID NO:24

GGT ACT TGT TTT CGG TAC TTT GGT GCT TTG GGA CCA CGG TTT GAT GGT GT

35

SEQ ID NO:25

TGC GCG GAG TTT CTA TTT GTG TAT GGC GTT CCT TAT CTA GGG CAG ACT TC

40

SEQ ID NO:26

TTT GTA CAG TGC TTT CGC TTG TCT TCG CAG CGC GCT AAT TGC TTG CGA GT

SEQ ID NO:27

GAG CTC AGT GGG GTC TTG GTA GGT TAG AAG AAG TAG CTA TGG CTT TCG AA

45

SEQ ID NO:28

CGT GAT AGC CCA CGG TCA AGG GTC TAC GAG TCA TTT GTT CCT AAC GCT GC

50

SEQ ID NO:29

CAA GGA GGA TAT ATG CTT GGG ATC AGT CGT GTT GTT GAT ATT TAT GAT GG

SEQ ID NO:30

55

AGG CTG CAG GCT TGG ATG GTG CTT CGG GGC GTC GTC TTA TTG CCT GCT AC

SEQ ID NO:31

GCC TCG GTG TGT TAA GGA GGA AGA GCG CCC ATC TCA GCA GTT ACC GGT CG

5

SEQ ID NO:32

CGC CCC GTC GAT TTG AAA CAC TCT TCA TCG GCG TTA ACC ACG GCG TGG AG

10

SEQ ID NO:33

CGG ACT GAG CAT TAG TTC GTG TCA CAG CGA CGT CGT TGT GTA AGG CTG AA

15

SEQ ID NO:34

TCC TGC CAA GCT CCT TTT TTT GGT AGT GAA TTT CCT TTA TCC TGG GGC GA

SEQ ID NO:35

20 CTA AAG TAT GTG TTA GTA TGG CCC TGC TTA TTA ATG TCG GGA GTT CGG ..

25

SEQ ID NO:36

TAG AAG CGT CGA ATC ATT GGG AAT TCG TGC ATT TAG GGC AGG CAC TTT GG

Target 3 (PROTOFIBRILS)

SEQ ID NO:37

TAA AGT GCG GAC TCA GGG AAT AAG GTG AGA ACT GAC CAA GGT GTG TGT TG

5

SEQ ID NO:38

TCG ACT TTT GAC AAG CAT CTC TTT TAC TGA GAG TTG GGA GGG AAC GGA TG

10

SEQ ID NO:39

GGG GTG CTA AGC ATT TGG CAT CCG TTT TGT GAA CTG CTC GAT GTT TAT TC

15

SEQ ID NO:40

TTA ACT GCA CCT TGC AGT AAC TAC AGG ATA GCA GTC CTA GAG CCA GTC AT

20

SEQ ID NO:41

TGC ATT ACC AGG GGA TAA CCT CGC ATT TGG CGG GTT AGG AGT AAC GTG CA

25

SEQ ID NO:42

ACT CTC GGT ATA TTG TTA GAT TGG GAG CGA CGC GTC ACC GTA TGA CAT GT

30

SEQ ID NO:43

GGT TAG CGG GGT TAC CTA ACA TCA GCT CTA GTT AGA CCT TTT TTT ACA AC

35

SEQ ID NO:44

CGA ATG CTT CGT AGT AAG TAA TGA ATC TTT TTG ACA CAC TAA TCG TAG GA

40

SEQ ID NO:44

GTC CCG TCC ATA GTG CTC GCC ACC ATT TCC TTT GGG TCA GGA ATT AGT TC

45

SEQ ID NO:45

TGG GAG AAG GAC TAG CTC GTT ATT GGT CAT GTT AGT CAT AGC CTG ACA CC

SEQ ID NO:46

CGG GGC ATA GTA CAG AAT CTT AGT GGG TGT TCT TTG ATT CTG GAG GAG CA

45

SEQ ID NO:47

GTG TGT TTT TAT CTA CTG GTC GGT GGT TTG GTT GGT AAT GCT TAA GCG GC

50

SEQ ID NO:48

TTG GAA CCC AGT GTG TTT TAC ACG CTC ATC TTT GCA ACA GGG TGT GTG AC

55

SEQ ID NO:49

ACG GTT AAC AAT CAT GGG CAA GCT CTT AGA ACA GCG TTC TGC GAT TTA CGA

SEQ ID NO:50

GAC GCC GCC GGG GAG CTC TAA ACG GAT TAC CAT TTG TCG GTG GTC TTA TT

5

SEQ ID NO:51

GCA TAG GAT TTC GGT TGG GAT AGA TAT TAT TCG GTT TCG ATC ATA CGT AT

10

SEQ ID NO:52

CTC ATA GGG ATG GTC TCC CGC TGG GCT TTT TCT GTT AAC ATT TAG AAC TC

15

SEQ ID NO:53

CAG GCC GCC GGG GAG CTC TAA ACG GAT TAC CAT TTG TCG GTG GTC TTA TT

SEQ ID NO:54

20

TCA CGT GTG CTG TAC GAC TGA TGT TTT TGC TGC CAG AATG ACT AGA AAT
GT

SEQ ID NO:55

25

ATC GTA AGT GAT TGT TGT TTT ACA TGG CCT CCA GTT GGG GAG TCT TCC AC

30

SEQUENCES OF CONSTANT FLANKING REGIONS (AT 5' AND 3'ENDS) OF
INSERTS5' end of top strand (primer 1) SEQ ID NO:56

35

5' AAT TAA CCC TCA CTA AAG GGA ACT GTT GTG AGT CTC ATG TCG AA.....

5' to 3' end of top strand (complementary of primer 2) SEQ ID NO:57

40

.....TTG AGC GTC TAG TCT TGT CTC CCT ATA GTG AGT CGT ATT

SEQUENCES OF SELECTED REGIONS OF APTAMERS AGAINST β 2m.

Primer 1 SEQ ID NO:58

AGTAATACGACTCACTATAGGGCCAAGCTTGCATGCCTGCAG

5

Primer 2 SEQ ID NO:59

GGTACCGAGCTCAGGTTCCC

SEQ ID NO:60

10 NATTAGGCGAACATAGTAGNGAAAGAAAGNACAGCANGAGGGCT

SEQ ID NO:61

15 GTTGGTTACCGCGTACAGTGAAACTCGGAAAGTTGAAGGGCAAATGGGAAC

15

SEQ ID NO:62

20 GAGCAGCACCGGGCACGGCGAACCTAAAATCGGAGGCCGGGTGCAGCATGTG
AC

20

SEQ ID NO:63

25 GGCTNTGACANGGCAGGATAGCCGGNCNANGCGANCNNINGNCCNCGANACCCGACNGT
GG

25

SEQ ID NO:64

30 GGTACCGAAAAGTCATTGGTTACAACCAGGCAGGCGCAGGAA

30

SEQ ID NO:65

GAATGGCGAGTTGAGCGACTGAGGCAGCATGGAATCATACGTAC

35

SEQ ID NO:66

GGAGGCCGAGAGGGCAGAACCCAGCGACGCGACGGAAAGACCATAACGGCAGC

40

SEQ ID NO:67

GCACACGGGCCGCACCCCTGCGAAACGACTATACGTCACTAGAGCAGGTTGCGGAGTCC
C

45

SEQ ID NO:68

GTGCGAGCAGGGCAACCAGAAGAAAACGTAGGTAGAGTGTGAGTTGATGAGACGT

SEQ ID NO:69

GCCGCAAGAACGGGAGAAGAGCGGAGAACGTTGAACCGACCGGAGG

50

SEQ ID NO:70

GTAGAGTGTGGCTAGCGTGACCAGACATCTACGTGGCAGGGAGCATTG

55

SEQ ID NO:71

GGAGGGGCCGTAAACGCGAACGAGACAACCAGATAAGGACCGCCCAATGAGAGGAACGGC
AA

pH3.6 induced β 2m fibrils (Immature Fibrils)

5 SEQ ID NO:72
AGTAATACGACTCACTATAAGGCCAAGCTTGCATGCCTGCAGATGAGAATACACAGAACAGGGAGAAGGGATGAATCAATAAGGTACACTAACCAACNCGGTACCGAGCTCAGGTT
CCC

10 SEQ ID NO:73
ATGAGAATACACAGAACAGAGGAGAAGGGATGAATCAATAAGGTACACTAACCAACNC
C

15 SEQ ID NO:74
AAAAATAAAANTGTGTACACNAAANNGCNANCCCNGGAANGAANGNCAACAAANGTNA
GT

20 SEQ ID NO:75
GGGAGAATTATGGAGTTTGIAAAACCATTGGTCAGTGGCAGAGGITCATCACCGTCATC

25 SEQ ID NO:76
ACACCTGGAATTAAATTCAAGGACACCCACCGCGCTACGAATAGAGCGGGAACGACGAC
C

30 SEQ ID NO:77
CGGAAGAGCACAAAAAAGGGACTCGCCTTGAAGGAACNTGC

35 SEQ ID NO:78
TTACGTCTGGCTNAACGAATGAACGGGGAAAGNAAGGAATGATTGGANCATANACAG
N

40 SEQ ID NO:79
GGAGTGTGGATATGA

45 SEQ ID NO:80
ACACGGAGGCACCTACAGTACTGGGCAGGAGTTGCGCAGAGGACTAGTGGAAAAGGAG
T

50 SEQ ID NO:81
GCCAGCACGACAAANAGCAGGACGTAAAGAAGACGAAAGGGAGAACATTGGGGAGAC
GA

55 SEQ ID NO:82
CCTGGGATCTCCAGGGGGCGGCGAGCGATAGGTGTGCGTGAGTTGAAAAGGCAGGGCA
A

SEQ ID NO:83
GAGACAAGTCGGTAGGACAGAGGAGTGAACAAAAGAAGCAGAGAGGAGTCAGAGCA
GC

5

SEQ ID NO:84
ATCTACCGGTTACAAATCAAGAGAACTATTTGTATGAGCCACTTATCTCCTGAAGT

10

SEQ ID NO:85
CGCANGAAATATAAACGTGGGGAGGACCAGGGAGAGTACTCCAAAGAGTGAAGAAGGT
T

15

SEQ ID NO:86
GCGGTAGAATGCATGGCGATTGCGATTGTAGGATTCCGCATCACACCTCC

20

SEQ ID NO:87
AAAAGGACAGGGAGC

25

SEQ ID NO:88
ACTATAAGTNAGNNGGAGGGGGANCATGAAACAATNGTTAAGAACGTANANTGGNTGA

30

SEQ ID NO:89
ACACGGAGGCACCTACAGTACTGGGCAGGAGTTCGCGAGAGGACTAGTGGAAAAGGAG
T

SEQ ID NO:90

AACGAAATGATAACAACAAATACACACGTACACCGAAGTTGACCCAAGACTC

Aptamers against β2m mature Fibrils

SEQ ID NO:91

5 ATTAACGAGANTGAAGGAAANCAGGGAGGGAGANCAGGCACAACGGCGACANGAAAAGA
GAGAGTGCAGTANCCG

SEQ ID NO:92

10 CCGAGGCCGCACACATAAGGGGGAGGGAAAGACAGCAGAATAANAGGAGGGCGATAGT
NC

SEQ ID NO:93

15 GGTAAGGTGGAAGGGAAAAGGAAACGGAATGAACCCCGTTATGGCCGAAAAGGGAC
GAACAGGACGCGTAGCCCTACGATCCA

20

SEQ ID NO:95

CGAGGACGAAANAGTTAGAAAAGGAGACGGCGTTCGAACGAACCATCCCCTAGGT

25

SEQ ID NO:96

AAGTGANNAGGCAAAAGGAAAAAAAAGGTGAACAAAGGCTGCTC

30

SEQ ID NO:97

GGCCCGACGAAGTGGGGGAGGAACGTTNGTGTGAGTGATTGGAGTNCCCTGGCGA
AATCC

35

SEQ ID NO:98

GCAAACGGGGCGTTCGCGGAGGAGTGGGAAGAAAAACGAGAGAAGAGTTGGAACG

40

SEQ ID NO:99

GCANGGGAANGGATTGAACGAGAAGAAGGAGGAGC

45

SEQ ID NO:100

GCACCTTCTCACTTNNGGCACAAACCGCGCACCGGGCTAGNCTGGAGTGGATGAA
CGAC

50

SEQ ID NO:101

TGAGGGGAGGTTGGCGCGAAGGCGAGGCAGCACGACCAGAAGTTTGAGTCGAGAGG
GGAT

55

SEQ ID NO:102

CCTGGAGGAGGGCAGCGNCAGAAGGGAAAAAGAAAAGAACTATTCTGGAGCGG
AT

SEQ ID NO:103

GAAAAGGAGGGGATTNAAATCGCGTGAAGGTGAATTGTTGCCAGGGGCGAATNCGG
T

5

SEQ ID NO:104

GGGGCTTCATNGAGAGAACGACAGACGAAAAAAAGGGGGGGNTCAAGAGGAA
GAGACCGA

10

SEQ ID NO:105

GTGTAAGCTTGCCTCGAAGATGAANAAAATGTCGAATCCTCGCTGTGCCGCCAGACGTGA

15

Downstream primer (SEQ ID NO:106)

[5' TAA TAC GAC TCA CTA TAG GGA GAC AAG ACT AGA CGC TCA A...3'] (SEQ ID NO:106)

20

Random 50 mer (SEQ ID NO:107).

[5' AAT TAA CCC TCA CTA AAG GGA ACT GTT GTG AGT CTC ATG TCG AA-N₅₀- TT GAG
CGT CTA GTC TTG TCT 3'].

25

JAN01P1 (SEQ ID NO:108)

5'AGT ATT ACG ACT CAC TAT AGG GCC AAG CTT GCA TGC CTG C'3

JAN01P2 (SEQ ID NO:109)

30 5'GGG AAC CTG AGC TCG GTA CC'3

JAN01T (SEQ ID NO :110)

5'CCA AGC TTG CAT GCC TGC AG N₆₀ GGT ACC GAG CTC GAA TTC CC'3

35 SEQ ID NO: 111

FYLLYYTE

SEQ ID NO:112

DWSFYLLYYTEFT

40

SEQ ID NO:113

DWSFYLLYYTEFTPTEKDEYA